#### Check for updates

#### OPEN ACCESS

EDITED BY Morad M. Mokhtar, Agriculture Research Center (ARC), Egypt

REVIEWED BY Achraf El Allali, Mohammed VI Polytechnic University, Morocco Ake Liu, Changzhi University, China Sridhar Malkaram, West Virginia State University, United States Honghe Sun, Cornell University, United States Xiujun Zhang, Chinese Academy of Sciences (CAS), China

CORRESPONDENCE You-Long Cao youlongchk@163.com Zhong-Jian Liu zjliu@fafu.edu.cn Wei-Sheng Wu wessonwu@ncku.edu.tw Wen-Chieh Tsai tsaiwc@mail.ncku.edu.tw

<sup>†</sup>These authors have contributed equally to this work

RECEIVED 09 October 2023 ACCEPTED 26 January 2024 PUBLISHED 20 February 2024

#### CITATION

Cao Y-L, Chen Y-Y, Li Y-L, Li C-I, Lin S-T, Lee B-R, Hsieh C-L, Hsiao Y-Y, Fan Y-F, Luo Q, Zhao J-H, Yin Y, An W, Shi Z-G, Chow C-N, Chang W-C, Huang C-L, Chang W-H, Liu Z-J, Wu W-S and Tsai W-C (2024) Wolfberry genome database: integrated genomic datasets for studying molecular biology. *Front. Plant Sci.* 15:1310346. doi: 10.3389/fpls.2024.1310346

COPYRIGHT

© 2024 Cao, Chen, Li, Lin, Lee, Hsieh, Hsiao, Fan, Luo, Zhao, Yin, An, Shi, Chow, Chang, Huang, Chang, Liu, Wu and Tsai. This is an open-access article distributed under the terms of the Creative Commons Attribution License (CC BY). The use, distribution or reproduction in other forums is permitted, provided the original author(s) and the copyright owner(s) are credited and that the original publication in this journal is cited, in accordance with accepted academic practice. No use, distribution or reproduction is permitted which does not comply with these terms.

# Wolfberry genome database: integrated genomic datasets for studying molecular biology

You-Long Cao<sup>1,2\*†</sup>, You-Yi Chen<sup>3†</sup>, Yan-Long Li<sup>1,2†</sup>, Chung-I Li<sup>4</sup>, Shao-Ting Lin<sup>5</sup>, Bing-Ru Lee<sup>6</sup>, Chun-Lin Hsieh<sup>6</sup>, Yu-Yun Hsiao<sup>7</sup>, Yun-Fang Fan<sup>1,2</sup>, Qing Luo<sup>1,2</sup>, Jian-Hua Zhao<sup>1,2</sup>, Yue Yin<sup>1,2</sup>, Wei An<sup>1,2</sup>, Zhi-Gang Shi<sup>1,2</sup>, Chi-Nga Chow<sup>8</sup>, Wen-Chi Chang<sup>8</sup>, Chun-Lin Huang<sup>9</sup>, Wei-Hung Chang<sup>10,11</sup>, Zhong-Jian Liu<sup>12,13,14\*</sup>, Wei-Sheng Wu<sup>6\*</sup> and Wen-Chieh Tsai<sup>5,7,8,15,16\*</sup>

<sup>1</sup>National Wolfberry Engineering Research Center, Ningxia Academy of Agriculture and Forestry Sciences, Yinchuan, China, <sup>2</sup>Institute of Wolfberry Engineering Technology, Ningxia Academy of Agriculture and Forestry Sciences, Yinchuan, China, <sup>3</sup>Department of Agronomy, National Chiayi University, Chiaiyi, Taiwan, <sup>4</sup>Department of Statistics, National Cheng Kung University, Tainan, Taiwan, <sup>5</sup>Graduate Program in Translational Agricultural Sciences, National Cheng Kung University and Academia Sinica, Tainan, Taiwan, <sup>6</sup>Department of Electrical Engineering, National Cheng Kung University, Tainan, Taiwan, 7Orchid Research and Development Center, National Cheng Kung University, Tainan, Taiwan, <sup>8</sup>Institute of Tropical Plant Sciences and Microbiology, National Cheng Kung University, Tainan, Taiwan, <sup>9</sup>Department of Biology, National Museum of Natural Science Taichung, Taiwan, <sup>10</sup>Department of Psychiatry, National Cheng Kung University Hospital, Collage of Medicine, National Cheng Kung University, Tainan, Taiwan, <sup>11</sup>Department of Psychiatry, National Cheng Kung University Hospital, Douliu, Taiwan, <sup>12</sup>Key Lab of National Forestry and Grassland Administration for Orchid Conservation and Utilization and International Orchid Research Center at College of Landscape Architecture, Fujian Agriculture and Forestry University, Fuzhou, Fujian, China, <sup>13</sup>Zhejiang Institute of Subtropical Crops, Zhejiang Academy of Agricultural Sciences, Wenzhou, China, <sup>14</sup>Institute of Vegetable and Flowers, Shandong Academy of Agricultural Sciences, Jinan, China, <sup>15</sup>Department of Life Sciences, National Cheng Kung University, Tainan, Taiwan, <sup>16</sup>University Center for Bioscience and Biotechnology, National Cheng Kung University, Tainan, Taiwan

Wolfberry, also known as goji berry or Lycium barbarum, is a highly valued fruit with significant health benefits and nutritional value. For more efficient and comprehensive usage of published L. barbarum genomic data, we established the Wolfberry database. The utility of the Wolfberry Genome Database (WGDB) is highlighted through the Genome browser, which enables the user to explore the L. barbarum genome, browse specific chromosomes, and access gene sequences. Gene annotation features provide comprehensive information about gene functions, locations, expression profiles, pathway involvement, protein domains, and regulatory transcription factors. The transcriptome feature allows the user to explore gene expression patterns using transcripts per kilobase million (TPM) and fragments per kilobase per million mapped reads (FPKM) metrics. The Metabolism pathway page provides insights into metabolic pathways and the involvement of the selected genes. In addition to the database content, we also introduce six analysis tools developed for the WGDB. These tools offer functionalities for gene function prediction, nucleotide and amino acid BLAST analysis, protein domain analysis, GO annotation, and gene expression pattern analysis. The WGDB is freely accessible at https:// cosbi7.ee.ncku.edu.tw/Wolfberry/. Overall, WGDB serves as a valuable resource for researchers interested in the genomics and transcriptomics of L. barbarum.

Its user-friendly web interface and comprehensive data facilitate the exploration of gene functions, regulatory mechanisms, and metabolic pathways, ultimately contributing to a deeper understanding of wolfberry and its potential applications in agronomy and nutrition.

#### KEYWORDS

wolfberry, *Lycium barbarum*, wolfberry genome database (WGDB), user-friendly, genomics, transcriptomics

### Background

Wolfberry, also known as goji berry or Lycium barbarum, is a bright red or orange-red berry that belongs to the Lycium genus. The Lycium genus comprises approximately 100 species that are distributed from temperate to subtropical regions. These plants have various adaptations, such as drought, salt, and temperature tolerance, which allow them to thrive in diverse environments (Yao et al., 2018). Wolfberry has been used in traditional Chinese medicine for centuries due to its numerous health benefits. In recent years, it has gained popularity worldwide as a superfood because of its rich nutritional profile and potential healthpromoting properties. Wolfberries are packed with essential nutrients and bioactive compounds, making them a valuable addition to a balanced diet. They are a rich source of vitamins, minerals, antioxidants, and phytochemicals (Vidović et al., 2022). Some of the prominent nutrients found in wolfberries include vitamin C, vitamin A, iron, zinc, fibre, zeaxanthin, and polysaccharides (Vidović et al., 2022).

While many researchers have focused on the functional ingredients and potential industrial applications of wolfberry, there has been increasing attention given to genetic and genomic approaches in understanding the molecular mechanisms of fruit development, nutrient accumulation, biosynthesis of bioactive compounds, physiological processes, and stress tolerance in wolfberry. For example, the transcriptional ratio of branch node structural genes F3'5'H/F3'H may determine the phenotypic difference in anthocyanin biosynthesis between L. ruthenicum and L. barbarum fruits (Zhen et al., 2014). Additionally, a study identified 137 R2R3-MYB genes in the wolfberry genome, and Lba11g0183 and Lba02g01219 were suggested as candidate R2R3-MYB genes regulating carotenoid biosynthesis in wolfberry (Yin et al., 2022). Another study compared the transcriptome, metabolome, and hormone changes between L. chinense and L. ruthenicum and found that ABA (abscisic acid) and flavones might play positive roles in resistance to salinity stress in wolfberry (Qin et al., 2022).

In 2021, the genome of wolfberry *L. barbarum* was sequenced using a whole-genome shotgun strategy and PacBio technology. This species has 24 chromosomes, and the assembled genome size is 1.67 Gb, with a contig N50 value of 10.75 Mb. High-throughput/resolution chromosome conformation capture (Hi-C) technology was adopted to obtain the lengths of the 12 chromosomes, which ranged from 106.53 to 172.84 Mb. In total, 33,581 genes and 151 miRNAs were annotated in the L. barbarum genome (Cao et al., 2021). Molecular biologists or agronomists who are interested in the wolfberry genome could access the genome sequences from the NCBI database. However, many of them might not have appropriate knowledge or analysis skills to explore the biological significance embedded in the genetic sequences. The WGDB encompasses not only the genome and transcriptome information of L. barbarum but also the annotated gene position at the specific location of the genome, functional annotation in various databases (structure database, GO, and KEGG database), transcriptional regulation (promoter and transcription factor), and posttranscriptional regulation (miRNA and target mRNA). Based on this dataset, a wolfberry L. barbarum database was established in this study to provide easy-to-use web interfaces for accessing this comprehensive information.

### **Methods**

#### Construction and content

The architecture of the WGDB is designed to store and analyze L. barbarum genome sequences and annotation data. It consists of several components: 1. MySQL 5.7 Database: This is used to store the collected L. barbarum genome sequences and their corresponding annotation data. MySQL is a popular open-source relational database management system. 2. Django 1.11.1 Application: Django is a Python web framework that handles the execution of all the analysis tasks in the WGDB. It provides a highlevel abstraction for building web applications. 3. Web Interface: The web interface of the WGDB is constructed using HTML and JavaScript. It allows the user to interact with the database, access and visualize the stored data, and perform various analysis tasks. 4. DataTables: WGDB utilizes the DataTables plugin in the jQuery JavaScript library to generate tables for displaying and interacting with data in the web interface. DataTables provide features such as sorting, searching, and pagination for efficient data presentation. 5. D3.js: To generate interactive plots of synteny and gene order, WGDB employs D3.js, a powerful JavaScript library for creating

10.3389/fpls.2024.1310346

dynamic and data-driven visualizations. D3.js enables the creation of custom visualizations based on the retrieved data.

The WGDB is deployed on a workstation running the Linux operating system, specifically Ubuntu 16.04.6. The hardware configuration of the workstation includes two CPUs, 55 GB RAM, and 3.6 TB of hard disk space. This setup allows for efficient storage, processing, and analysis of large and complex biological datasets. Figure 1 shows an overview of the database architecture. In addition to the mentioned components, the WGDB integrates various data and tools summarized in Table 1. These resources include genome browsers such as JBrowse for navigating and visualizing L. barbarum genomes, as well as additional databases such as BLAST for sequence similarity searches. Overall, the WGDB serves as an open-access and web-available portal that simplifies the workflow for analyzing and visualizing the genomes of L. barbarum and related transcriptome information.

#### The database content

*L. barbarum* has a karyotype of 2N = 2X = 24 chromosomes. The assembled genome total length is 1.67 Gb with an N50 value of 10.75 Mb, which encompasses 12 pseudomolecules (Cao et al., 2021). We also evaluated assembly continuity of the *L. barbarum* genome by PlantLAI (https://bioinformatics.um6p.ma/PlantLAI), and got the raw LAI score 12.67 and the LAI value 12.22 of the assembled genome. This results indicated the *L. barbarum* genome is a reference quality genome (Ou et al., 2018; Mokhtar et al., 2023). The 33,581 protein-coding genes were predicted and assigned a specific Gene ID to serve as a unique identifier. These Gene IDs enable the investigation of annotated functions of individual genes. The WGDB allows the user to select specific genes and explore their annotated functions, particularly those related to biological processes of interest.

The database also includes transcriptomics data obtained from RNA sequencing (RNA-seq) experiments performed on *L. barbarum*. The RNA-seq data were derived from various developmental stages

TABLE 1	Summary	of data	and	tools	that	could	be	browsed	and	used	for
the Wolfk	berry (Lyci	um bark	arur	n).							

Genome browser	Scaffold ID, Scaffold sequence, Gene model
Gene annotation	Gene ID, Gene sequence, BLAST top hit descriptions, KEGG pathway, GO terms, Interpro description, Pfam description, Swissprot description, TrEMBL description, Number of predicted target genes from Arabidopsis and rice
Transcriptome	Gene ID, FPKM and TPM values in various tissues
Metabolism pathway	Gene ID, Genes mapped to the KEGG pathways
Tools	
Browse tools	IntrPro ID, InterPro description, Pfam ID, Pfam description, GO terms, GO description, Matrix ID, Gene ID from Arabidopsis and rice, Number of predicted target genes
Nucleotide blast	BLASTN, tBLASTX, tBLASTN
Protein blast	BLASTX, BLASTP
Domain search	Pfam ID, Pfam description, Searching for related genes ID
GO search	GO terms, GO description, Searching for related genes ID
Gene expression profile	Gene ID, FPKM and TPM values in various tissues, Heat map, expression pattern, PCA, Cluster

of flowers and fruits, mature leaves, flowers, stems, and roots. The RNA-seq data that had been sequenced in triplicate for each collected sample were downloaded from PRJNA788208 at NCBI. Clean reads of each sample were assessed by FastQC (version 0.12.1). The R package Rsubread (version 2.16.0) was used to map the *clean* reads in the fastq files to the reference genome and calculate the raw read count matrix. The clean read counts were then mapped to the predicted genes, and transcripts per million (TPM) and fragments per kilobase of transcript per million mapped reads (FPKM) values



were calculated. These TPM and FPKM values represent the gene expression levels in different tissues and developmental stages. The integration of gene expression data into the WGDB enables the user to analyze and explore gene expression patterns in *L. barbarum*.

Overall, the WGDB provides access to a wide range of data, including the *L. barbarum* genome assembly, predicted genes and miRNAs, gene annotations, and gene expression information derived from RNA-seq experiments. This comprehensive collection of data facilitates the study of *L. barbarum* biology and the exploration of gene functions and regulatory mechanisms in this species.

## Utility and discussion

The WGDB is a highly efficient, web-accessible relational database with comprehensive genomic information. Through the

web interface, the genome information of *L. barbarum* in the database could be freely obtained. The information can be linked via the "https://cosbi7.ee.ncku.edu.tw/Wolfberry/" website (Figure 2).

**Genome Browser**: The Genome browser interface allows the user to explore the *L. barbarum* genome and browse the sequences of specific chromosomes. In the first step, the user enters the *L. barbarum* genome into the Genome browser interface (Figure 2, step 1). The user can select one of the chromosomes they want to explore. This selection allows them to focus on a specific chromosome's sequences (Figure 2, step 2). After selecting a chromosome, the user can zoom in or zoom out on the genome sequence (Figure 2, step 3). Zooming in allows for a closer view of the DNA sequence, while zooming out provides a broader overview. To navigate through the genome, the user can utilize the "arrowhead" feature. Clicking on the arrowhead allows the user to



move along the genome sequence, either forwards or backwards, to browse different positions (Figure 2, step 4). While browsing the genome, the user can identify regions containing genes. They can move the cursor to a specific gene of interest and perform various actions (Figure 2, step 5). By clicking the right button of the mouse, the user can retrieve the gene sequence associated with the selected gene. This action might display the nucleotide sequence or provide a downloadable file containing the gene's DNA sequence (Figure 2, steps 6 to 7). Alternatively, the user may choose to highlight the gene of interest. This action visually distinguishes the gene from the surrounding sequence, making it easier to identify and analyze (Figure 2, steps 8 to 9). By combining these features, the user can navigate the *L. barbarum* genome, explore specific chromosomes, zoom in or out, browse positions, and access gene sequences or highlight genes for further analysis.

Gene annotation: The gene annotation process involves accessing various pieces of information about genes within L. barbarum. The BLASTP programs were used to select the best hit in the NR or TrEMBL database with the smallest E-value, and the Evalue must be less than 10<sup>-5</sup>. The user could access the information of the genes in this page (Figure 3, step 1). To retrieve information about a specific gene, the user can enter the Gene ID into a search box (Figure 3, step 2). This ID serves as a unique identifier for the gene of interest. Upon querying the Gene ID, the user can access the gene sequence linked to that particular ID (Figure 3, steps 3-4). This sequence could be displayed or made available for download. To determine the specific location of the gene on the chromosome, the user can retrieve the gene's location information (Figure 3, steps 5-6). These data provide the chromosome number and the position of the gene within that chromosome. The user can access the expression profile of the gene (Figure 3, steps 7-10). The user can retrieve the best BLAST hit in the NCBI database, which refers to the gene's closest matching sequence in the NCBI database (Figure 3, steps 11-12). The accession number allows the user to access additional information about this hit. The user can explore the gene's involvement in a biological pathway using the KEGG pathway database (Figure 3, steps 13-15). This information helps understand the role of genes within a specific biological context. The gene's function can be classified using gene ontology (GO) terms (Figure 3, steps 16-17). GO terms provide standardized annotations that describe the gene's functional attributes. The KEGG and GO pathways of a wolfberry gene are annotated using the KEGG and GO pathways of its orthologues in Arabidopsis. The orthologues in Arabidopsis for a wolfberry gene are assigned by the best hit of running BLASTP against all Arabidopsis protein sequences. The best hit is defined as the one with the smallest Evalue, and the E-value must be less than 10<sup>-5</sup>. The user can access information about functional protein domains associated with the gene using resources such as Interpro, Pfam, or Swisspro (Figure 3, steps 18-23). These domains provide insights into protein structure and function. The Pfam/InterPro domains of a wolfberry protein were identified using HMMER/InterProScan tools (Quevillon et al., 2005). Similar to the NCBI database, the user can retrieve the best BLAST hit in the EMBL-EBI database (Figure 3, steps 24-25). This hit provides additional information and context for the gene of interest. The user can explore the gene's regulation by transcription

factors and their binding sites within the promoter. This information may be available for both Arabidopsis and rice orthologues (Figure 3, steps 26-29). This study provides insights into the regulatory mechanisms controlling gene expression. The promoter of a wolfberry gene is defined as the 2,000 bp upstream of the start codon of a gene. The binding sites of all Arabidopsis/rice (transcription factors) TFs in a given promoter were identified using the promoter analysis tool in PlantPAN 3.0 (Chow et al., 2019). After running the promoter analysis tool, all the Arabidopsis/ rice TFs whose binding sites at the promoter of a wolfberry gene of interest could be screened. Then, the best hits of L. barbarum TFs in Arabidopsis/rice were identified by BLASTP. Finally, we recommended that these Wolfberry TFs might bind to the promoter of a Wolfberry gene of interest. By following these steps, the user can gather comprehensive information about genes, including their sequences, locations, expression profiles, database hits, pathway involvement, functional classifications, protein domains, regulatory factors and binding sites.

Transcriptome: The transcriptome feature within the interface allows the user to explore the expression patterns of genes. The user can click on the "Transcriptome" option (Figure 4, step 1) to navigate to the Transcriptome page. This page provides information about gene expression. On the Transcriptome page, the user can select the expression level metric they want to use, either TPM (transcripts per million) or FPKM (fragments per kilobase of transcript per million mapped reads) (Figure 3, steps 2-3). These metrics are commonly used normalization methods in RNA sequencing (RNA-seq) data analysis. It helps to account for differences in sequencing depth and gene length across samples. TPM values represent the relative abundance of a transcript in a sample (Zhao et al., 2020). FPKM is similar to TPM but uses the concept of fragments instead of transcripts (Zhao et al., 2021). The Gene ID associated with each gene can be linked to its annotation (Figure 3, steps 4-5). This allows the user to access additional information about the selected genes, such as gene function, biological pathways, or protein domains. The Transcriptome page provides a search function at the top right of the page (Figure 3, steps 6-7). The user can enter a specific Gene ID into the search box to retrieve the gene expression patterns for the searched gene. This allows the user to quickly find and analyze the expression of a specific gene of interest. Overall, the transcriptome feature provides the user with the ability to explore gene expression patterns. The user can select between TPM and FPKM as expression level metrics, link Gene IDs to gene annotations, and utilize the search function to retrieve expression patterns for specific genes.

**Metabolism pathway:** The "Metabolism pathway" page within the interface provides information about selected genes involved in KEGG pathways. The user can navigate to the "Metabolism pathway" page to explore metabolic pathways and their associated genes (Figure 5, step 1). On the "Metabolism pathway" page, the user can select one of the major pathways and then choose a specific subpathway of interest (Figure 5, steps 2-3). These pathways represent different metabolic processes or branches within metabolism. Once a pathway and subpathway are selected, the user can choose one or multiple Gene IDs associated with genes in that pathway. Clicking the "View" icon (Figure 5, steps 4-8) allows



the user to generate an image that shows the selected pathway, with enzymes involved in the pathway marked in red. This image is derived from the KEGG database. The generated colored pathway image is interactive (Figure 5, step 9). The user can interact with the image to access the KEGG database and explore additional information about the enzymes, pathways, and related metabolic processes. This feature allows the user to delve deeper into the specific metabolic pathways and their associated genes. Overall, the "Metabolism pathway" page enables the user to explore metabolic pathways and the involvement of selected genes within those pathways. The user can select major pathways and subpathways, view pathway images with marked enzymes, and access the KEGG database for further exploration and information retrieval.

**Tools:** We developed six tools for the analysis of the *L. barbarum* genome and gene function. These tools encompass various functionalities to assist the user in their analysis (Figure 6



step 1). Under the "Browse tools" section, there are five subtools available. These subtools offer different approaches to analyze the genome and gene function of L. barbarum (Figure 6, step 2). In the case of the "Domain-InterPro" tool, the user can either browse each page or input an InterPro domain ID or InterPro domain keyword. This tool allows the user to search for specific InterPro domains related to their analysis. As an example, the keyword "YABBY" is input (Figure 6, steps 3 to 5). When the user clicks on the InterPro ID (blue color), they will be directed to the InterPro database, where they can access detailed information about the InterPro domain they selected. This step helps the user obtain comprehensive information about the domain they are interested in (Figure 6, steps 6 to 7). Additionally, the page provides a whole genome analysis of the genes encoding the indicated domain. This feature allows the user to explore and analyze the genes associated with the selected InterPro domain across the entire L. barbarum genome (Figure 6, steps 8 to 9). Finally, the steps involved in using the "Domain-Pfam" and "GO Term" tools are similar to the process described for the "Domain-InterPro" tool. The user can follow the instructions provided, likely involving searching for specific domains or terms, accessing detailed information, and conducting genome-wide analyses (Figure 6, steps 10 to 22). Overall, these tools offer a range of functionalities for analyzing the L. barbarum genome and gene function, with specific features for searching, obtaining domain details, and conducting genome-wide analyses related to InterPro domains, Pfam domains, and GO terms.

All the genes encoding transcription factors have been identified, and their binding sites in the *L. barbarum* genome and orthologues in *Arabidopsis* and rice were also predicted as well as their putative target genes. The user can click on either "TF-*Arabidopsis thaliana*" or "TF-*Oryza sativa*" to access the respective pages. These pages contain information about the identified transcription factors and their characteristics (Figure 7, steps 1 to 4). The predicted binding sites of *L. barbarum* transcription factors are linked to PlantPAN 3.0

(Chow et al., 2019). Clicking on the binding site redirects the user to the PlantPAN 3.0 database, where they can access additional information and analysis related to the predicted binding sites (Figure 7, steps 5 to 6). The orthologues of Arabidopsis or rice for the identified L. barbarum transcription factors are indicated (Figure 7, steps 7 to 8). This information helps the user understand the relationships and similarities between the transcription factors in different plant species. The table includes a column labelled "Number of predicted target genes". This column provides the count of predicted downstream genes that are regulated by the transcription factor encoded by the L. barbarum gene. The user can click on the number in the column to proceed to further analysis (Figure 7, steps 9 to 11). Clicking on the specific number of predicted target genes navigates the user to a table that presents the predicted target gene IDs (Figure 7, step 11). This table helps the user identify and explore the specific genes regulated by the transcription factor of interest. By clicking on a specific target gene ID, the user can access information about the transcription factor genes that regulate the target gene (Figure 7, step 12). The information provided for each target gene includes the binding sequence of the transcription factor that regulates it (Figure 7, step 13). Additionally, the position of the binding sequence within 2,000 bp upstream of the target gene promoter is indicated (Figure 7, steps 14 to 17). These details help the user understand the regulatory mechanisms involved in the interaction between transcription factors and their target genes. In summary, the tools we have developed allow the user to explore and analyze the transcription factors in L. barbarum, including their predicted binding sites, orthologues in Arabidopsis and rice, and putative target genes. The provided functionalities enable the user to delve into the regulatory relationships between transcription factors and their targets in a convenient and effective manner.

In the tools for nucleotide BLAST and protein BLAST, the user can input a nucleotide sequence or a protein sequence to search for sequence fragments of *L. barbarum*. These sequences could be



pasted into the designated area within the tools (Figures 8, 9, steps 1 to 4). After performing the BLAST search, a BLAST result page is presented. This page displays detailed information about the sequence alignment, allowing the user to examine how the input sequence aligns with the *L. barbarum* genome or protein sequences (Figures 8, 9, steps 5 to 7). The user can find the gene annotation on the BLAST result page (Figures 8, 9, steps 8 to 9). This information provides insights into the annotated genes

associated with the sequence fragments of interest in *L. barbarum.* The BLAST result page also allows the user to select any of the hit sequences to view their expression profiles. The user could find expression data for the selected sequences, which can provide valuable insights into their transcriptional activity or abundance across different conditions (Figures 8, 9, steps 10 to 11). On the expression profile page, the user can select the transcriptomes and genes they want to compare. They can

	Homej	page	erry (Lycium	barbarum) Ge	enome Database				Prov	vse t	OOIS Select to	ool in t	his page	
	Home Genome be	arowser 🛢 Ger	About Wolf	Transcriptome	Metabolism pathway	F Taols Contai Browse tools	at 👔 Help	13	10 4	17			ins page	
			Wolfberry is in species in tempe environments. T	n the genus <i>Locious L</i> . I state and subtropical in the plant usually have	Solaraceae 1 to regions allo 1 to beautiful flowers red a	Nucleotide BLAST (r	olaste, thiasts; thiaste) ta blastal	InterPro ID 4	~	(4) En	iter InterPro	) ID or	Keyword	ex. YABBY
	XXX "	beek ?	artificial planting red color fruit, n	en species en aranje o thorns, and grows u	ck here			IPR00001			Ninga Ratinoid X receptor/HNF4			0
	CAN	2	renpos. Congrue areas. Ningxia Pr being first bred I However, Lr-goji	rovince is the center of here. Lr-goji has dark t has many thorns, mai	of origin for Lb goj, with black colored fruit with king picking difficult, a	GO search Gene expression pro	.ele	199200000 199200007			Metallathiosen, vertebrate Tubby, C-lorminal			13
	S.S.	1.00	Many kinds of Chinese wolfber	s. Lo-goji, is distribute active compounds ha ry, including polysacc	ed in all over the China. we been detected from the harides (LBPs), zeasarthi	e fruit, leaves and n in ester, flavonoids, i	oots of alkaloids,	1PR000000		Po	C2 domain min phosphatase 2A regulatory subur	nt PR56		4
<complex-block></complex-block>	Lycian barbaran		A number of stua have a variety of anti-inflammato	dies in particularly she pharmacological prop ry, anti-servescence, n	owed that LBPs are the m perfies, such as immune n europrotective, anti-infe	ain active ingredien regulation, as well as crive, aphrodisiac, a	essential ons. its, and they antioxidant, nti-tumor and	IPR000010			Cystelin-domain Ubiquitin/SCMO-activating enzyme E1	1-lika		2
			Early in 2011, of Ningvia Acade sequence the wh	the wolfberry (Lection env of Agriculture and role genome and prov	<ul> <li>Jurisense) genome prog d Forestry, Yinchuan of C ide the reference genetic manufacturing</li> </ul>	ject was initiated by hina. The project de information to plan	the institute dicated to et biologists.	IPR000012			Retroval VpR-VpX protein Peptidase M7, snapelysin			0
<complex-block></complex-block>			broubers retrict	orist, and natural pha	rhacologist.			Sice 10 • entres	-					
	5 Sho	w th	e In	terPr	OID:	and	descrip	tion 🤇	7 L	ink 1	to Inter	Pro		
	Domain - InterPro	Domain - Pfam	GO Term TF	<ul> <li>Arabidopsis_thalian</li> </ul>	a TF - Oryza_sativa				<b>\$</b>	InterPro	Classification of protein fam			
	Search: YAEBY						Designer		Home #/Brees	Search     E     (Dy Entry / InterPro	Income • Results Relea	ase notes Do	swelcad + Help	+ About
<complex-block></complex-block>	InterPro ID *			Description			Total gene number in th	e gennee 0	F	YABBY	protein <sup>®</sup> IPROD	06780		
	PROSE780 Show	Click	here	YABBY protei	n		8 🖈			InterProtectry	Short name: 14687			
	Showing 1 to 1 of 1 ent	tries (filtered from 4	40,101 total entries	1)			Click here	1 Next		Proteins 4x	Description	and a local second	and a feature factor	er instant in disease erset
	9 Dro	wide	ne ma	oro d	otoilo	d inf	ormotic	n	Dorsain	Architectures 41 Tourscores 75	leaf, shoot and flower der	velopment <sup>[]], 2</sup>	.11	
		- ue	OCUS Name	0 analysis		re accession	Signature d	iscription Ø	Star	t location 0	Stop location \$	Previou Score	s 1 Next Sean	nc ( InterPro ID
	View Interpro	Lba01g	02578	Ptam	PF04590		YABBY protein		11		162	2.3E-65	YABBY protein	IPR006780
	View Interpro	Lbat2g	00512	Ptam	PF04690		YABBY protein	1770	30		165	6.95-47	YABBY protein	IPR006780
<complex-block></complex-block>	View Interpro	Lba04g	02927	PANTHER	PTHR31675 PF04690		PROTEIN YABBY 6-REI YABBY protein	AIED	1		205	6.8E-88 1.5E-67	YABBY protein YABBY protein	IPR006780 IPR006780
	View Interpro	Lba06g	01391	Ptam	PF04650		YA88Y protein		11		165	9.35-58	YABBY protein	IPR006780
Note:	View Interpro	Lbattig	00381	Pfam	PF04530		YA68Y protein		12		171	7.75-70	YABBY protein	199006780
<complex-block></complex-block>	View Interpro	Lba06g	00382	Ptem	PF04690		YABBY protein		13		169	1.10-69	YABBY protein	1PR006780
	View Interpro	Lba06g	00495	Ptam	PF04690		YABBY protein		8		156	7.3t5-68 9.6E-62	YABBY protein	IPR006780
				· •			• .•		-	T * 1	4 6.			
<complex-block></complex-block>	<sup>12</sup> Sho	ow th	ie pf	am I	D and	l des	cription	L	14	LINK	to prai	m	_	
<complex-block></complex-block>	Domain - InterPro	Domain - Ptern	GO Tern	TF - Arabidopsis_th	aliana TF - Oryza_s	ativa			Fami	ily: YABB	Y (PF04690)		21 a	chitectures 2062 sequences
<complex-block></complex-block>	Transfer Valley			Enter I	nterPro I	D or Ke	eyword (ex. 1	ABBY)	Domain	organisation	Summary: YABBY p Mare includes annotations and	orotein additional femily	r information from a range	e of different sources. These sour
<complex-block></complex-block>	Pfan ID *			Description		0	Previo Total gene number in th	e genome 0	Alignme HMM lo	ents po	No Wikipedia article Pfai	m InterPro		
<complex-block></complex-block>	PF04880			YA68Y protein			15 🔿 '		Trees Curatio	n & model	this tab will be gradually replace	oed by the Wikip	edia tab.	ease. As we make is using mus
<text></text>	Showing 1 to 1 of 1	entries (Fitneed fro	orn 17,929 total en	tries)			Click here	s 1 Next	Structu	res .	WART proteins are a group of	plant-specific tra	ansoription involved in the	specification of abasial polarity
<complex-block></complex-block>	Due			d	.4	J :f	·		trRoset	ta Structure	1. Beeman 3L; , Curr Opin	Plant Biol 2000;	3:17-22.: The VABBY ger	e family and abaxial cell fate. B
Image: Normal biology         Contract of the state	Show 10 v entrie	"	5 III0	ore u	etane	u IIII	ormatic	711					Search	
www.m       www.m <td< td=""><td>Link *</td><td>gene name 🕴</td><td>Pfam 10 (</td><td>Envelop start</td><td>Drivelop end</td><td>\$ Alignment</td><td>t start \$ Alignment end</td><td>♦ HMM start Ø</td><td>HWM end</td><td>target nar</td><td>ne \$ description of tary</td><td>get \$ is</td><td>ndependent Evalue</td><td>conditional Evalue</td></td<>	Link *	gene name 🕴	Pfam 10 (	Envelop start	Drivelop end	\$ Alignment	t start \$ Alignment end	♦ HMM start Ø	HWM end	target nar	ne \$ description of tary	get \$ is	ndependent Evalue	conditional Evalue
Langend       Finde 1       <	View Pfam	Lba02g00512	PF04690.13	29	163	30	165	2	101	YABBY	YABBY protein	1.899	19999999999999976-48	1.1e-52
wight	View Pfam	Lba04g00457	PF04690.13	14	176	15	176	2	162	YABBY	YABBY protein	1.299	0999999999999996e 64	1.399999999999999999966-68
window	View Pfam	Lba04g02927	PF04690.13	18	167	19	167	2	162	YABBY	YABBY protein	7.899	1999999999999999 68	8.8999999999999999999999
	View Pfam	Lba05g01391	PF04990.13 PF04990.13	9	170	11	166	3	158	YABBY	YABBY protein	16-58	1 1999000000000000000000000000000000000	1.0999999999999999996 62
	View Pfam	Lbe06g00382	PF04990.13	12	169	13	169	2	162	YABBY	YABBY protein	0.499	199995559999995e-70	4.7999999999999999999
we w	View Pfam	Lbe06g02226	PF04590.13	58	216	60	216	3	162	YABBY	YABBY protein	2.099	199999999999994e-67	1.509999999999999999976-71
	View Pfam	Lbs07g00495	PF04090.13	T	160	8	156	2	152	YABBY	YADBY protein	4.399	nnnnnnnnn5e-62	2.5e-66
Image: Section of the section of t	Sang tovoren	ow t	ha C	ים חי	) and	doco	rintion			<b>.</b> .	1.00			Previous 1 Neo
Image: Section of the section of t	<b>9</b> 511	υνι	nec	JO II	) anu	uesc	ription			9 Lii	ik GO			
Image: Section of Se		Domain - Pfa	m GO Term	TF - Arabidopsis_)	thaliana TF - Oryza,	aativa			(8	AmiGO 2	Home Search - Browse	Tools & Res	cerces Help Feed	aed. About
Instrume         Instrume           0         Excertise         20 <td>Domain - InterPro Please type ID or i</td> <td></td> <td>_<u>/</u>_"</td> <td>Enter</td> <td>GO ID or</td> <td>· Keywo</td> <td>ord (ex. GO:(</td> <td>1009908)</td> <td></td> <td></td> <td></td> <td>flov</td> <td>ver develo</td> <td>nment</td>	Domain - InterPro Please type ID or i		_ <u>/</u> _"	Enter	GO ID or	· Keywo	ord (ex. GO:(	1009908)				flov	ver develo	nment
Image: Second	Domain - InterPro Please type ID or i Bearch: GO:0000	9908			escription		( Tota	gene number in				nor		pinon
	Domain - InterPho Please type ID or i Bearch: GO:0009 GO ID *	9908		D				and permit	Terr	n Information <b>O</b>	908			
Image: Second	Domain - InterPro Please type ID or Id Bearch: G0700000 G0 ID A G070000000	9408		fowe	r development		22.5	22						
Inter Unitation         Same	Domain - InterPro Please type ID or I Bearch: G0:00099 G0 ID A G0:0000000 Show 10 J A Showing 1 to 1 of	20 1 entise (Barod I	Click he	ere ere	r development		Click	here Nat		Name flower de Ontology biological prioriyes None	velopment _process			
Line         Line/Long         Southers         Southers <thsouthers< th="">         Southers         <th< td=""><td>Donain - Interfeo Please type ID or I Starch: GOXXXX GOXXXX Show 10 - 14 Showing 11 51 of 23</td><td>20 1 entise (libered l</td><td>Click he</td><td></td><td>e development</td><td>d in</td><td>22 s Click</td><td>here Nat</td><td>a Ab</td><td>Name flower de Ontology biological promytris None mate IDs GC 0045</td><td>velopment Lancess 409</td><td></td><td></td><td></td></th<></thsouthers<>	Donain - Interfeo Please type ID or I Starch: GOXXXX GOXXXX Show 10 - 14 Showing 11 51 of 23	20 1 entise (libered l	Click he		e development	d in	22 s Click	here Nat	a Ab	Name flower de Ontology biological promytris None mate IDs GC 0045	velopment Lancess 409			
Marco Dam         Margonia	Demain - travefile Pesses type 1D or 1 Sourch: GO0000 00 ID + GO000000 Drow 10 - A Browing 1b 1 of 20 Processor	ece 20 1 action (Barod I ovid)	Click he from 47,347 lobal o <b>es m</b>	ere strives)	e development	ed in	Click formati	here Not	A Ala	Name Rowerde Ontology biological pronyms None mate IDs GC 0040	velopment L process		Search	
Marco Tam         Indeptify         None Recurrent         Configure           Vaca Co Tam         dop003         none Recurrent         dop003           Vaca Co Tam         dop004         none Recurrent         dop004           Vaca Co Tam         dop004         none Recurrent         dop004	Denain - Hoards Passet tipe 1D or 1 Dearch: G000000 G0 ID 0 Drow 10 0 Drow 10 0 Showing 1 b 1 of Showing 1 b 1 of Showing 1 b 1 of Showing 1 b 1 of	esce	Click he teen 47,347 load e <b>es m</b> Leek	ere erre torre d	e development	ed in	22 s Click formati	≥22 here Noot ON	A Ata	Name flower de Ontolegy biological promyms None mate IDs GC 0049 Go Na	velopment jancess 400	•	Search	со н
Name of Design         Name of Design         Name of Design           Visite Or Sim         Langkrith?         Noor Mexiquent         0.000000	Denain - Interfeo Please type ID or I Search G00000 00 ID - Interfeo Down 50 - Showing 1 Ib 1 of Showing 1 Ib 1 of of Showing 1 Ib 1 of Showing 1 of Showing 1 of Showing 1 of Showing 1 of Showing 1 of Showing 1 of Showing 1 of Showing 1 of Showing 1 of Showing 1 of Showing 1 of Showing	esee	Click he tom 47,347 total o <b>ES M</b> Link	ere erre orre	e development	ed in	22) 5 Click formati	here Nost ON forer dev	A Ata	Marme Rower do Denzelegy biological processes None mate IDs GC 20145 GO No	viloprent Ljucces	¢	Search	co u
Max 60 Tem         Mark 50 Tem	Denain - Interfes Pease type ID or I Search (00000 00 D 1 Down 10 0 Down 10	20 ( 1 extras (Broad I ovide es	Click he from 47,347 lotel e es m	ere erries	r davelopment	ed int	22) 5 Click formati	23 here Nost On Rouer dev Rouer dev Rouer dev	A & & Atte	Marne Rover de Deretelagy biologica procytes Nove mate IDs GC 2049 Go Ni	vitigment jacoses	•	Search 20 0009906 30 0009906 30 0009906	COM
Value CO Tamin         Lab/Gr140         Nover development         0.000000           Value CO Tamin         Lab/Gr100         Nover development         0.000000           Value CO Tamin         Lab/Gr2010         Nover development         0.000000	Densin - Harffor Rease type ID of V Dense type ID of V Dense ID of V Den	20 20 1 eterse (Eleved ovid	Click he from 47,347 lotal es m Lint	ere erries)	e davalopement letaile Lawo 1 gccoso Lawo 2 gcco	ed int	22) Click Click formati	Nover devi nover devi nover devi nover devi nover devi	A 8 Alla	Marree Rover do Onterlegy biological processor Nove made IDs GC 0040	vilignent Jacoss 409		Search 20 0009906 30 0009906 30 0009906	00 M
Unset of Lamity         Lamity/site         Rest reference         Constraint         <	Bersan - Interfej           Beass type ID or M           Beass type ID or M           Beass type ID or M           Boweng ID or M           Mew CO Term           Mew CO Term           Mew CO Term	20 20 1 extense (Kilawad I ovid	Click he tron 47,347 total e <b>ES M</b>		Lbartgorsen	ed in:	22 c Click formati	Nover devi fourer devi fourer devi fourer devi fourer devi fourer devi fourer devi	A stapment stopment stopment stopment	Maree flower do doctology biotropy yrocrywis None mate IDE GC 0045 GO No	viloprati 600 Ma	¢ c c c c c c	Search 20 0009966 30 0009966 30 0009966 30 0009966	60 M
Muse 00 Tem         Muse designed         0.000960           Muse 00 Tem         Languards         Know designed         0.000960           Muse 00 Tem         Languards         Know designed         0.000960	Bersan - Interfej           Beass type ID or M           Beass type ID or M           Beass type ID or M           Boxes ID or M           Memory ID or M     <	20 ( 1 eters (lieved) 0 vid	Click he bon-47,347 table es m Lant	ere erresi IOTE C	r davatopresent	ed int	Click formati	Next Next Next Next Next Next Next Next	A 8 American Ropment Ropment Ropment Ropment	Mares Reversa biological processos biological processos Biol Galacias Go Na	vilonent 1.000 100 100 100 100 100 100 100 100 1		Search 20 0009906 30 0009906 30 0009906 30 0009906 30 0009906	GO 14
New 60 Tem         Lba 10;02275         four development         00 000006	Bersan-Isarking     Rease type 10 or 1     Rease type 10	20 Contraction of the second s	Click he from 47,347 total e <b>es m</b> Lunt	ere ere iorred	r drevelopment Electable Laborgorison Lab	ed in:	22 s Click formati	Next Next Next Next Next Next Next Next	A standard stand Standard standard stan Standard standard stand Standard standard stand Standard standard stand Standard standard standard standard standard standard standard standard	Mare Revelop Biological provpets Nore made Dis GL2040 Co N	vilenent 1.000 100 100 100 100 100 100 100 100 1	• 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	Search 20 0009968 20 0009968 20 0009968 20 0009968 20 0009968 20 0009968	a0 ki
	Bersan - Isarking           Bersan - Isarking           Bears type ID or 1           Box or 10           Box or 10           Brows ID or 10           Brows ID or 10           Brows ID or 10           Meer CO-Term	20 ( 1 defas (Bowl ovid	Click he ton 47,347 total o es m	ere ere ere ere ere ere ere ere ere ere	r dividipment Categorian Lastigorian Lastigorian Lastigorian Lastigorian Lastigorian Lastigorian Lastigorian Lastigorian Lastigorian Lastigorian	ed in:	22 s Click formati	Net	A somet somet somet somet somet somet somet somet somet	Maren Develop biological provpers Nore manis Bio Col 0640 Co No	vilaginant : 2000		Search 20 0009666 30 0009666 30 0009666 30 0009666 30 0009666 30 0009666 30 0009666	со и

choose metrics such as TPM (transcripts per million) or FPKM (fragments per kilobase of transcript per million mapped reads) to quantify gene expression. Clicking on "refresh" initiates the comparison process (Figures 8, 9, steps 12 to 15). The expression profile page offers various ways to visualize the comparison results, such as a heatmap, bar chart, principal component analysis (PCA), or hierarchical clustergram. The

user can choose the preferred visualization method based on their needs and preferences (Figures 8, 9, steps 16 to 24). Overall, the Nucleotide BLAST and Protein BLAST tools allow the user to search for sequence fragments in the *L. barbarum* genome or predicted proteome. The tools provide detailed sequence alignment information, gene annotation, and expression profiles for the hit sequences. Additionally, the



expression profile page offers multiple visualization options to facilitate the analysis and interpretation of the comparison results.

The Domain search tool allows the user to search for sequences or keywords associated with specific Pfam or Interpro IDs. The user can enter a query by sequence, gene ID, or keyword (Figure 10, steps 1 to 6). The tool takes the user's input and performs a search based on the specified sequence, gene ID, or keyword and processes the query and identifies relevant Pfam or Interpro IDs associated with the input. Then, the tool presents the search results to the user, displaying the identified Pfam or Interpro IDs that match the query (Figure 10, step 7). The search result webpage allows the user to choose one of three methods, Jaccard, intersection, or union (Figure 10, step 8), which is performed by similarity comparison and then determines how the domains are screened for inclusion in the query. Using the selected



method, the tool filters the Pfam or Interpro domains and presents the refined list to the user (Figure 10, step 9). The user can click on a specific Pfam or Interpro ID to access the corresponding domain's characteristics (Figure 10, steps 10 to 11). From the domain characteristic page, the user has the option to select several Pfam or Interpro IDs to search for similar genes (Figure 10, steps 12 to 14). The user can further select a gene ID from the search results to access the

transcriptomic data associated with the genes (Figure 10, steps 15 to 20). In the new page, the user could choose a heatmap, bar chart, PCA, or hierarchical clustergram to visualize the expression patterns of the selected genes (Figure 10, steps 21 to 29). This comprehensive tool enables the user to search for domains, explore domain characteristics, find similar genes, and analyze the transcriptomic data of selected genes using various visualization methods.



For the gene ontology (GO) search, the user enters the GO ID in the search box to query the gene ontology (Figure 11, steps 1 to 2). The tool processes the query and retrieves the relevant search results. The search result webpage displays the retrieved results (Figure 11, step 3). The user could select one of three methods, Jaccard, intersection, or union, to filter the GO ID results accordingly (Figure 11, step 4). Then, the user could click the GO ID to visit the interested GO characteristic to explore GO annotation and gather information about the selected GO ID (Figure 11, steps 5 to 6). The user has the option to select the GO ID for searching similar genes. The tool performs a search based on the selected GO ID and retrieves genes with similar annotations (Figure 11, steps 7 to 9). The user could also use keywords to query the GO content (Figure 11, steps 10 to 12). The user can select one of the similarity comparison methods to filter the GO content results (Figure 11, step 13). The user can further select several GO



IDs for searching similar genes (Figure 11, steps 14 to 16). After obtaining the list of similar genes, the user can further select several gene IDs for analysis (Figure 11, steps 17 to 20). The tool retrieves the transcriptomic data for the selected genes. In the new page, the user has the option to choose from different visualization methods such as a heatmap, bar chart, PCA plot, or hierarchical clustergram (Figure 11, steps 21 to 29). This GO search tool allows the user to query by GO ID or keyword, explore GO characteristics and

annotations, find similar genes based on GO annotations, and analyze the transcriptomic data of selected genes using various visualization methods.

The database also provides a tool for analyzing the expression profiles of the user's genes of interest (Figure 12, step 1). The user enters specific gene IDs in the provided box to retrieve the transcriptomic data for those genes (Figure 12, steps 2 to 3). The user has the option to select either TPM or FPKM as the expression



evaluation method (Figure 12, step 5) and choose spatial and temporal expression items for analysis (Figure 12, steps 6 to 7). After acquiring the expression data, the user can select a visualization method, such as a heatmap, bar chart, PCA, or hierarchical clustergram, to display the expression profiles (Figure 12, steps 8 to 16). This tool enables the user to analyze the expression profiles of their genes of interest by inputting specific gene IDs, selecting expression evaluation methods, considering spatial and temporal expression aspects, and visualizing the expression data using different visualization options.



#### A case study

*L. barbarum* has gained popularity as a "superfood" due to its potential health benefits. One of the key components that contributes to their nutritional value is their carotenoid content. Carotenoids participate in a wide range of plant physiological processes, including light harvesting, photosynthesis, plant growth, and responses to biotic and abiotic stresses (Xiong et al., 2019). We are interested in the regulation of carotenoid biosynthesis in *L. barbarum*, and we investigated the possible genes involved in *L. barbarum* carotenoid production. It has been

shown that carotenoids are synthesized through the plastid methylerythritol phosphate (MEP) pathway and positively regulated by the WRKY transcription factor in tomato fruit (Yuan et al., 2022). Because *L. barbarum* and tomato are classified in the same Solanaceae family, it is reasonable to predict that carotenoids accumulated in *L. barbarum* fruit might be regulated in a similar way. First, we identified the *L. barbarum* orthologous gene (*Lba02g01426*) of the tomato *1-deoxy-D-xylulose 5-phosphate synthase* gene (*SlDXS1*) via BLASTP, the gene encoding the enzyme that produces 1-deoxy-D-xylulose 5-phosphate from glyceraldehyde-3-phosphate (GAP) and pyruvate in the MEP pathway for isoprenoid biosynthesis. Then, we went to the gene annotation page and entered Lba02g01426 to query its detailed annotation (Figure 13, steps 1 to 2). Three hundred forty-one transcription factors that putatively regulate *Lba02g01426* expression could be seen (Figure 13, step 3). After clicking the 341 TF marked in red, we could then see the thirty-eight genes encoding WRKY transcription factors that might bind to the promoter of *Lba02g01426* (Figure 13, steps 4 to 5). WRKY transcription factors have been reported to control carotenoid accumulation in several dicot plants, such as sweet osmanthus, citrus, and tomato (Han et al., 2016; Jiang et al., 2019; Duan et al., 2022; Yuan et al., 2022). Click WRKY (38), and we could see the predicted WRKY list (Figure 13, step 6). Because *Lba03g01218* is the orthologue of tomato *SlWRKY35*, we could select this gene and find its binding site (Figure 13, steps 7 and 8). The binding site shown here is highly similar to that of tomato SlWRKY35 (Yuan et al., 2022). Overall, our investigation provides valuable insights into the potential regulation of carotenoid biosynthesis in *L. barbarum* and highlights the involvement of WRKY transcription factors as potential regulators of this process.

# Conclusion

Although several genomic databases related to Solanaceae have been reported, such as the Solanaceae Genomic Network



(Fernandez-Pozo et al., 2014), PoMaMo (Meyer et al., 2005), PepperHub (Liu et al., 2017), and *Nicotiana attenuata* Data Hub (Brockmöllere et al., 2017), the genome database of wolfberry is still absent. Thanks to advanced sequencing technology, the *L. barbarum* genome has been successfully sequenced (Cao et al., 2021). Our WGDB provides an integrative public platform for sharing and analyzing research data and easy-to-use web interfaces. The availability of WGDB will facilitate various studies related to wolfberry, such as understanding its genetics, identifying genes responsible for specific traits or functions, and exploring potential applications in agriculture, biotechnology, and pharmacology. Researchers interested in wolfberry biology will now have easy access to data and a user-friendly interface to explore, analyze, and gain insights into the molecular aspects of this plant.

## Data availability statement

The raw data and whole genome–assembled scaffold sequences for the Licium barbarum (PRJNA640228), (https://www.ncbi.nlm.nih.gov/ bioproject/?term=PRJNA640228) were downloaded from the National Center for Biotechnology Information (NCBI) database. The transcriptome data were downloaded from PRJNA788208, (https:// www.ncbi.nlm.nih.gov/bioproject/?term=PRJNA788208).

## Author contributions

W-CT: Conceptualization, Formal analysis, Funding acquisition, Project administration, Resources, Supervision, Writing - original draft, Writing - review & editing. Y-LC: Data curation, Funding acquisition, Project administration, Resources, Supervision, Validation, Writing - review & editing. Y-YC: Data curation, Formal analysis, Investigation, Methodology, Validation, Writing review & editing. Y-LL: Data curation, Formal analysis, Investigation, Methodology, Project administration, Resources, Validation, Writing - review & editing. C-IL: Data curation, Investigation, Methodology, Software, Validation, Writing - review & editing. S-TL: Methodology, Validation, Writing - review & editing. B-RL: Data curation, Methodology, Software, Visualization, Writing - review & editing. C-LH: Data curation, Methodology, Software, Visualization, Writing - review & editing. Y-YH: Data curation, Formal analysis, Investigation, Validation, Writing - review & editing. Y-FF: Data curation, Formal analysis, Methodology, Validation, Writing - review & editing. QL: Data curation, Methodology, Validation, Writing review & editing. J-HZ: Data curation, Investigation, Validation, Writing - review & editing. YY: Data curation, Formal analysis, Validation, Writing - review & editing. WA: Data curation, Formal analysis, Investigation, Writing - review & editing. Z-GS: Data curation, Investigation, Validation, Writing – review & editing. C-NC: Data curation, Methodology, Validation, Writing – review & editing. W-CC: Formal analysis, Investigation, Methodology, Validation, Writing – review & editing. C-LH: Data curation, Formal analysis, Investigation, Writing – review & editing. W-HC: Investigation, Writing – review & editing. Z-JL: Conceptualization, Funding acquisition, Investigation, Resources, Supervision, Validation, Writing – review & editing. W-SW: Conceptualization, Formal analysis, Funding acquisition, Methodology, Software, Supervision, Validation, Visualization, Writing – original draft, Writing – review & editing.

# Funding

The author(s) declare financial support was received for the research, authorship, and/or publication of this article. Publication costs was funded by the Ministry of Science and Technology, Ningxia (NGSB-2021-2-01, 2021BEF02002-02), the Ministry of Science and Technology, Taiwan (MOST 111-2313-B-006-003-, MOST 110-2313-B-006-002-MY3, MOST 110-2622-B-006-009-, and MOST-111-2221-E-006-151-MY3), National Key R&D Program of China (Grant No. 2019YFD1000400), and National Natural Science Foundation of China [no. 31870199]. The funders have no role in the design of the study and collection, analysis, and interpretation of data and in writing the manuscript.

# Acknowledgments

We thank National Center for High-performance Computing (NCHC, https://www.nchc.org.tw) to kindly provide the cloud space for storage and assessment of transcriptomic data.

# Conflict of interest

The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

## Publisher's note

All claims expressed in this article are solely those of the authors and do not necessarily represent those of their affiliated organizations, or those of the publisher, the editors and the reviewers. Any product that may be evaluated in this article, or claim that may be made by its manufacturer, is not guaranteed or endorsed by the publisher.

# References

Brockmöllere, T., Ling, Z., Li, D., Gaquerel, E., Baldwin, I. T., and Xu, S. (2017). Nicotiana attenuata Data Hub (NaDH): an integrative platform for exploring genomic, transcriptomic and metabolomic data in wild tobacco. *BMC Genomics* 18, 79. doi: 10.1186/s12864-016-3465-9

Cao, Y., Li, Y., Fan, Y. F., Li, Z., Yoshida, K., Wang, J. Y., et al. (2021). Wolfberry genomes and the evolution of Lycium (Solanaceae). *Commun. Biol.* 4, 671. doi: 10.1038/ s42003-021-02152-8

Chow, C. N., Lee, T. Y., Hung, Y. C., Li, G. Z., Tseng, K. C., Liu, Y. H., et al. (2019). PlantPAN3.0: a new and updated resource for reconstructing transcriptional regulatory networks from ChIP-seq experiments in plants. *Nucleic Acids Res.* 47, D1155–D1163. doi: 10.1093/nar/gky1081

Duan, X., Jiang, C., Zhao, Y., Gao, G., Li, M., and Qi, H. (2022). Transcriptome and metabolomics analysis revealed that CmWRKY49 regulating CmPSY1 promotes  $\beta$ -carotene accumulation in orange fleshed oriental melon. *Hortic. Plant J.* 8, 650–666. doi: 10.1016/j.hpj.2022.07.005

Fernandez-Pozo, N., Menda, N., Edwards, J. D., Saha, S., Tecle, I. Y., Strickler, S. R., et al. (2014). The Sol Genomics Network (SGN)—from genotype to phenotype to breeding. *Nucleic Acids Res.* 43, D1036–D1041. doi: 10.1093/nar/gku1195

Han, Y., Wu, M., Cao, L., Yuan, W., Dong, M., Wang, X., et al. (2016). Characterization of OfWRKY3, a transcription factor that positively regulates the carotenoid cleavage dioxygenase gene OfCCD4 in Osmanthus fragrans. *Plant Mol. Biol.* 91, 485–496. doi: 10.1007/s11103-016-0483-6

Jiang, C. C., Zhang, Y. F., Lin, Y. J., Chen, Y., and Lu, X. K. (2019). Illumina® sequencing reveals candidate genes of carotenoid metabolism in three pummelo cultivars (Citrus maxima) with different pulp color. *Int. J. Mol. Sci.* 20, 2246. doi: 10.3390/jims20092246

Liu, F., Yu, H., Deng, Y., Zheng, J., Liu, M., Ou, L., et al. (2017). PepperHub, an informatics hub for the chili pepper research community. *Mol. Plants.* 10, 1129–1132. doi: 10.1016/j.molp.2017.03.005

Meyer, S., Nagel, A., and Gebhardt, C. (2005). PoMaMo - a comprehensive database for potato genome data. *Nucleic Acids Res.* 33, D666–D670. doi: 10.1093/ nar/gki018

Mokhtar, M. M., Abd-Elhalim, H. M., and El Allali, A. (2023). A large-scale assessment of the quality of plant genome assemblies using the LTR assembly index. *AoB Plants* 15, 1–8. doi: 10.1093/aobpla/plad015

Ou, S., Chen, J., and Jiang, N. (2018). Assessing genome assembly quality using the LTR Assembly Index (LAI). *Nucleic Acids Res.* 46, e126. doi: 10.1093/nar/gky730

Qin, X., Yin, Y., Zhao, J., An, W., Fan, Y., Liang, X., et al. (2022). Metabolomic and transcriptomic analysis of Lycium chinese and L. ruthenicum under salinity stress. *BMC Plant Biol.* 22, 8. doi: 10.1186/s12870-021-03375-x

Quevillon, E., Silventoinen, V., Pillai, S., Harte, N., Mulder, N., Apweiler, R., et al. (2005). InterProScan: protein domains identifier. *Nucleic Acids Res.* 33 (Web Server issue), W116–W120. doi: 10.1093/nar/gki442

Vidović, B. B., Milinčić, D. D., Marčetić, M. D., Djuriš, J. D., Ilić, T. D., Kostić, A. Z., et al. (2022). Health benefits and applications of Goji berries in functional food products development: a review. *Antioxidants* 11, 248. doi: 10.3390/antiox11020248

Xiong, C., Luo, D., Lin, A., Zhang, C., Shan, L., He, P., et al. (2019). A tomato B-box protein SIBBX20 modulates carotenoid biosynthesis by directly activating PHYTOENE SYNTHASE 1, and is targeted for26S proteasome-mediated degradation. *New Phytol.* 221, 279–294. doi: 10.1111/nph.15373

Yao, R., Heinrich, M., and Weckerle, C. S. (2018). The genus Lycium as food and medicine: A botanical, ethnobotanical and historical review. *J. Ethnopharmacol.* 212, 50–66. doi: 10.1016/j.jep.2017.10.010

Yin, Y., Guo, C., Shi, H., Zhao, J., Ma, F., An, W., et al. (2022). Genome-wide comparative analysis of the R2R3-MYB gene family in five Solanaceae species and identification of members regulating carotenoid biosynthesis in wolfberry. *Int. J. Mol. Sci.* 23, 2259. doi: 10.3390/ijms23042259

Yuan, Y., Ren, S., Liu, X., Su, L., Wu, Y., Zhang, W., et al. (2022). SlWRKY35 positively regulates carotenoid biosynthesis by activating the MEP pathway in tomato fruit. *New Phytol.* 234, 164–178. doi: 10.1111/nph.17977

Zhao, S., Ye, Z., and Stanton, R. (2020). Misuse of RPKM or TPM normalization when comparing across samples and sequencing protocols. *RNA* 26, 903–909. doi: 10.1261/rna.074922.120

Zhao, Y., Li, M. C., Konaté, M. M., Chen, L., Das, B., Karlovich, C., et al. (2021). TPM, FPKM, or normalized counts? A comparative study of quantification measures for the analysis of RNA-seq data from the NCI patient-derived models repository. *J. Transl. Med.* 19, 269. doi: 10.1186/s12967-021-02936-w

Zhen, S., Wu, M., Zho, C., Lin, X., Shen, X., Hayward, A., et al. (2014). Comparative analysis of anthocyanin biosynthesis during fruit development in two Lycium species. *Plant Physiol.* 150, 505–516. doi: 10.1111/ppl.12131